WHAT IS CLAIMED IS:

1. An isolated regulatory element that is capable of driving transcription in a seed-preferred manner, wherein said regulatory element comprises a nucleotide sequence selected from the group consisting of:
   a) sequences natively associated with DNA coding for maize Jip1, maize mi1ps3, or maize Lec1;
   b) the nucleotide sequences set forth in SEQ ID NOS: 1, 4, 7, or 10;
   c) a sequence that hybridizes to any one of SEQ ID NOS: 1, 4, 7, or 10 under highly stringent conditions;
   d) a sequence having at least 65% sequence identity to SEQ ID NO: 1, 4, 7, or 10, wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters.

2. An isolated regulatory element that is capable of driving transcription in a seed-preferred manner, wherein said regulatory element comprises a nucleotide sequence natively associated with DNA coding for any one of maize Jip1, maize mi1ps3, or maize Lec1.

3 The isolated regulatory element of claim 2, wherein said regulatory element comprises a nucleotide sequence natively associated with DNA coding for maize Jip1.

4. The isolated regulatory element of claim 2, wherein said regulatory element comprises a nucleotide sequence natively associated with DNA coding for maize mi1ps3.

5. The isolated regulatory element of claim 2 wherein said regulatory element comprises a nucleotide sequence natively associated with DNA coding for maize Lec1.

6. An isolated regulatory element that is capable of driving transcription in a seed-preferred manner, wherein said regulatory element comprises a nucleotide sequence set forth in any one of SEQ ID NOS: 1, 4, 7, or 10.

7. The isolated regulatory element of claim 6, wherein said regulatory element comprises a nucleotide sequence set forth in SEQ ID NO: 1.

8. The isolated regulatory element of claim 6, wherein said regulatory element comprises a nucleotide sequence set forth in SEQ ID NO: 4.

9. The isolated regulatory element of claim 6, wherein said regulatory element comprises a nucleotide sequence set forth in SEQ ID NO: 7.

10. The isolated regulatory element of claim 6, wherein said regulatory element comprises a nucleotide sequence set forth in SEQ ID NO: 10.

11. An isolated regulatory element that is capable of driving transcription in a seed-preferred manner, wherein said regulatory element comprises a sequence that hybridizes to any one of SEQ ID NOS: 1, 4, 7, or 10 under highly stringent conditions.

12. The isolated regulatory element of claim 11 wherein said regulatory element comprises a sequence that hybridizes to SEQ ID NO: 1 under highly stringent conditions.

13 The isolated regulatory element of claim 11 wherein said regulatory element comprises a sequence that hybridizes to SEQ ID NO: 4 under highly stringent conditions.

14. The isolated regulatory element of claim 11 wherein said regulatory element comprises a sequence that hybridizes to SEQ ID NO: 7 under highly stringent conditions.

15. The isolated regulatory element of claim 11 wherein said regulatory element comprises a sequence that hybridizes to SEQ ID NO: 10 under highly stringent conditions.

16. An isolated regulatory element that is capable of driving transcription in a seed-preferred manner, wherein said regulatory element comprises a sequence having at least 65% sequence identity to SEQ ID NOS: 1, 4, 7, or 10, wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters.

17. The isolated regulatory element of claim 16 wherein said regulatory element comprises a sequence having at least 65% sequence identity to SEQ ID NO: 1 wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters.

18. The isolated regulatory element of claim 16 wherein said regulatory element comprises a sequence having at least 65% sequence identity to SEQ ID NO: 4 wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters.

19. The isolated regulatory element of claim 16, wherein said regulatory element comprises a sequence having at least 65% sequence identity to SEQ ID NO: 7 wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters.

20. The isolated regulatory element of claim 16 wherein said regulatory element comprises a sequence having at least 65% sequence identity to SEQ ID NO: 10 wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters.

21. An expression cassette comprising a regulatory element and a first nucleotide sequence operably linked to the regulatory element, wherein the regulatory element is capable of initiating seed-preferred transcription of the first nucleotide sequence in a plant cell, wherein the regulatory element comprises a second nucleotide sequence selected from the group consisting of:

a) the nucleotide sequences set forth in any one of SEQ ID NOS: 1, 4, 7, or 10;

b) nucleotide sequences having at least 65% sequence identity to SEQ ID NOS: 1, 4, 7, or 10, wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters; and

c) a sequence that hybridizes to any one of SEQ ID NOS: 1, 4, 7, or 10, under highly stringent conditions.

22. The expression cassette of claim 20, wherein the regulatory element comprises a second nucleotide natively associated with DNA coding for maize Jip1 (jasmonate-induced protein), maize mi1ps3 (myo-inositol-1-phosphate synthase 3), or maize Lec1 (leafy cotyledon 1).

23. The expression cassette of claim 22 wherein the regulatory element is a nucleotide sequence natively associated with maize mi1ps3, is capable of expressing the first nucleotide sequence in an embryo-preferred manner.

24. The expression cassette of claim 20, wherein the regulatory element comprises a second nucleotide sequence comprising a nucleotide sequence set forth in SEQ ID NOS: 1, 4, 7, or 10.

25. The expression cassette of claim 20, wherein the regulatory element comprises a second nucleotide sequence comprising a nucleotide sequence having at least 65% sequence identity to SEQ ID NO: 1, 4, 7, or 10, wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters.

26. The expression cassette of claim 20, wherein the regulatory element is capable of initiating seed-preferred transcription of the first nucleotide sequence in a plant cell, wherein the regulatory element comprises a second nucleotide sequence that hybridizes to any one of SEQ ID NOS: 1, 4, 7, or 10 under highly stringent conditions.

27. A transformation vector comprising an expression cassette, the expression cassette comprising a regulatory element and a first nucleotide sequence operably linked to the regulatory element, wherein the regulatory element is capable of initiating seed-preferred transcription of the first nucleotide sequence in a plant cell, wherein the regulatory element comprises a second nucleotide sequence selected from the group consisting of:

a) the nucleotide sequences set forth in SEQ ID NOS: 1, 4, 7, or 10;

b) nucleotide sequences having at least 65% sequence identity to SEQ ID NO 1, 4, 7, or 10, wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters; and

c) a nucleotide sequence that hybridizes to any one of SEQ ID NOS: 1, 4, 7, or 10, under highly stringent conditions.

28. A plant stably transformed with an expression cassette comprising a regulatory element and a first nucleotide sequence operably linked to the regulatory element, wherein the regulatory element is capable of initiating seed-preferred transcription of the first nucleotide sequence in a plant cell, wherein the regulatory element comprises a second nucleotide sequence selected from the group consisting of:

a) the nucleotide sequences set forth in SEQ ID NOS: 1, 4, 7, or 10;

b) nucleotide sequences having at least 65% sequence identity to SEQ ID NOS: 1, 4, 7, or 10, wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters; and

c) a nucleotide sequence that hybridizes to any one of SEQ ID NOS: 1, 4, 7, or 10, under highly stringent conditions.

29. The plant of claim 28, wherein said plant is a monocot.

30. The plant of claim 29, wherein said monocot is maize, wheat, rice, barley, sorghum, or rye.

31. Seed of the plant of claim 28.

32. A method for selectively expressing a nucleotide sequence in a plant seed, the method comprising transforming a plant cell with a transformation vector comprising an expression cassette, the expression cassette comprising a regulatory element and a first nucleotide sequence operably linked to the regulatory element, wherein the regulatory element is capable of initiating seed-preferred transcription of the first nucleotide sequence in a plant cell, wherein the regulatory element comprises a second nucleotide sequence selected from the group consisting of:

a) the nucleotide sequences set forth in SEQ ID NOS: 1, 4, 7, or 10;

b) nucleotide sequences having at least 65% sequence identity to SEQ ID NOS: 1, 4, 7, or 10, wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters; and

c) a nucleotide sequence that hybridizes to any one of SEQ ID NOS: 1, 4, 7, or 10, under highly stringent conditions.

33. The method of claim 31 wherein the regulatory element is capable of initiating transient expression of the first nucleotide sequence in callus tissue.

34. The method of claim 32 further comprising regenerating a stably transformed plant from said transformed plant cell; wherein expression of said nucleotide sequences alters the phenotype of said plant seed.

35. The method of claim 32, wherein said first nucleotide sequence encodes a gene involved in fatty acid synthesis.

36. The method of claim 32, wherein said first nucleotide sequence encodes a gene having enhanced amino acid content.

37. A plant cell stably transformed with an expression cassette comprising a regulatory element and a first nucleotide sequence operably linked to the regulatory element, wherein the regulatory element is capable of initiating seed-preferred transcription of the first nucleotide sequence in a plant cell, wherein the regulatory element comprises a second nucleotide sequence selected from the group consisting of:

a) the nucleotide sequences set forth in SEQ ID NOS: 1, 4, 7, or 10;

b) nucleotide sequences having at least 65% sequence identity to SEQ ID NOS: 1, 4, 7, or 10, wherein the % sequence identity is based on the entire sequence and is determined by GAP version 10 analysis using default parameters; and

c) a nucleotide sequence that hybridizes to any one of SEQ ID NOS: 1, 4, 7, or 10, under highly stringent conditions.

38. The plant cell of claim 37, wherein said plant cell is from a monocot.

39. The plant cell of claim 38, wherein said plant cell is from maize, wheat, rice, barley, sorghum, or rye.

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add B5